Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG.1A

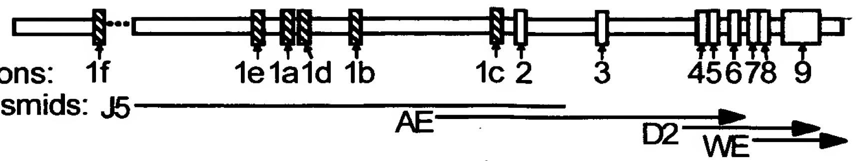

FIG.1B

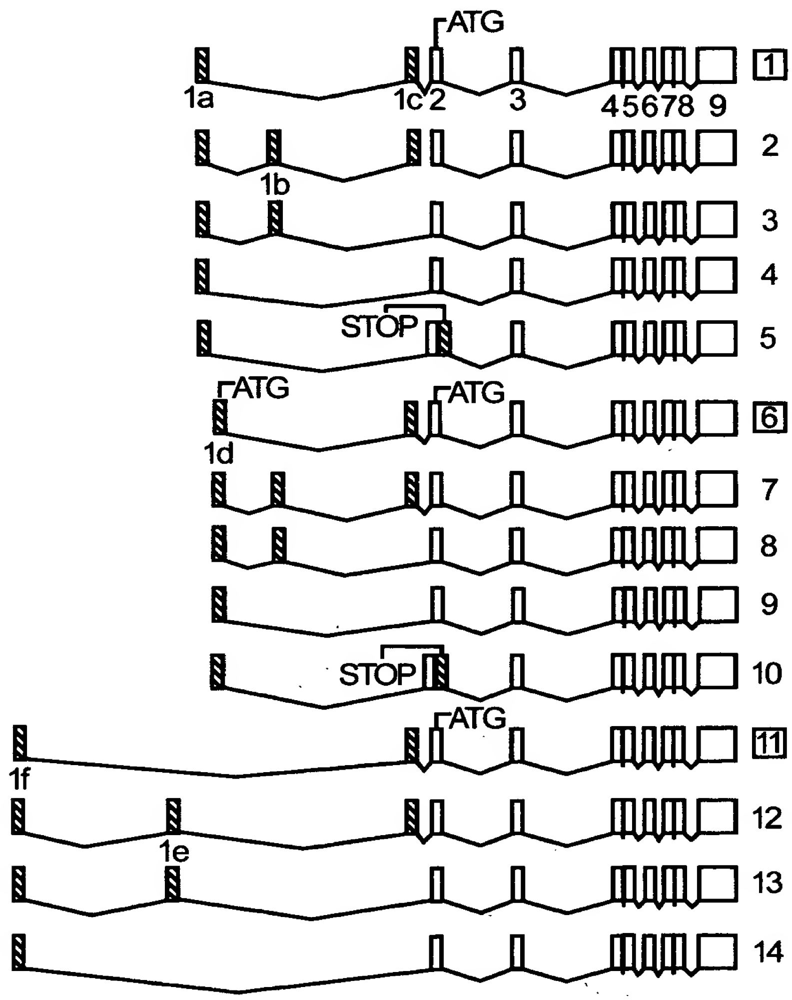

FIG. 1C

Transcript 1: MEAMA ASTSL PDPGD FDRNV PRI $\boxed{\text{DBD}}$ 427aa (SEQ ID NO.14)

Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI $\boxed{\text{DBD}}$ 477aa (SEQ ID NO.15)

Transcript 9: MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNV PRI $\boxed{\text{DBD}}$ 450aa (SEQ ID NO.16)

FIG. 4

A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO: 13)

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO: 6)

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGC$\boxed{\text{ATG}}$GAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCG$\boxed{\text{ATG}}$GTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)

FIG. 5A

Transcript 6
(Sequence Range: 1 to 1463)

```
        10         20         30         40         50
    *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                              MetGluTrpArg AsnLysLys>

        60         70         80         90        100
    *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

       110        120        130        140        150
    *    *     *    *     *    *     *    *     *    *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
 PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

       160        170        180        190        200
    *    *     *    *     *    *     *    *     *    *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

       210        220        230        240        250
    *    *     *    *     *    *     *    *     *    *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

       260        270        280        290        300
    *    *     *    *     *    *     *    *     *    *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
 GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

       310        320        330        340        350
    *    *     *    *     *    *     *    *     *    *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

       360        370        380        390        400
    *    *     *    *     *    *     *    *     *    *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

FIG. 5B

```
      410        420        430        440        450
   *     *     *     *     *     *     *     *     *     *
 CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
 GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
  HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

      460        470        480        490        500
   *     *     *     *     *     *     *     *     *     *
 AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
 TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

      510        520        530        540        550
   *     *     *     *     *     *     *     *     *     *
 CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
 GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
 LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

      560        570        580        590        600
   *     *     *     *     *     *     *     *     *     *
 GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
 CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
  SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

      610        620        630        640        650
   *     *     *     *     *     *     *     *     *     *
 AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
 TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

      660        670        680        690        700
   *     *     *     *     *     *     *     *     *     *
 CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
 GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
 ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

      710        720        730        740        750
   *     *     *     *     *     *     *     *     *     *
 CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
 GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
  ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

      760        770        780        790        800
   *     *     *     *     *     *     *     *     *     *
 TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
 AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

      810        820        830        840        850
   *     *     *     *     *     *     *     *     *     *
 AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
 TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
 SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```

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Application No.: 09/509,482
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FIG. 5C

```
        860       870       880       890       900
    *    *    *    *    *    *    *    *    *    *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

        910       920       930       940       950
    *    *    *    *    *    *    *    *    *    *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

        960       970       980       990      1000
    *    *    *    *    *    *    *    *    *    *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

       1010      1020      1030      1040      1050
    *    *    *    *    *    *    *    *    *    *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

       1060      1070      1080      1090      1100
    *    *    *    *    *    *    *    *    *    *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

       1110      1120      1130      1140      1150
    *    *    *    *    *    *    *    *    *    *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

       1160      1170      1180      1190      1200
    *    *    *    *    *    *    *    *    *    *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
 LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

       1210      1220      1230      1240      1250
    *    *    *    *    *    *    *    *    *    *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

       1260      1270      1280      1290      1300
    *    *    *    *    *    *    *    *    *    *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```

FIG. 5D

```
       1310       1320       1330       1340       1350
         *    *     *    *     *    *     *    *     *    *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
 GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

       1360       1370       1380       1390       1400
         *    *     *    *     *    *     *    *     *    *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

       1410       1420       1430       1440       1450
         *    *     *    *     *    *     *    *     *    *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

       1460
         *    *
TGAGATCTCC TGA (SEQ ID NO:2)
ACTCTAGAGG ACT (SEQ ID NO:17)
 GluIleSer ***>(SEQ ID NO:9)
```

FIG. 6A

Transcript 9
(Sequence range: 1 to 1382)

```
        10        20        30        40        50
    *    *    *    *    *    *    *    *    *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                               MetGluTrpArg AsnLysLys>

        60        70        80        90       100
    *    *    *    *    *    *    *    *    *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

       110       120       130       140       150
    *    *    *    *    *    *    *    *    *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

       160       170       180       190       200
    *    *    *    *    *    *    *    *    *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

       210       220       230       240       250
    *    *    *    *    *    *    *    *    *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

       260       270       280       290       300
    *    *    *    *    *    *    *    *    *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
 MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

       310       320       330       340       350
    *    *    *    *    *    *    *    *    *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

       360       370       380       390       400
    *    *    *    *    *    *    *    *    *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

FIG. 6B

```
         410         420         430         440         450
      *    *     *    *     *    *     *    *     *    *
  GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
  CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
   ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

         460         470         480         490         500
      *    *     *    *     *    *     *    *     *    *
  ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
  TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
 AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

         510         520         530         540         550
      *    *     *    *     *    *     *    *     *    *
  CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
  GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
  LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

         560         570         580         590         600
      *    *     *    *     *    *     *    *     *    *
  CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
  GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
   GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

         610         620         630         640         650
      *    *     *    *     *    *     *    *     *    *
  CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
  GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
 SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

         660         670         680         690         700
      *    *     *    *     *    *     *    *     *    *
  TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
  AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
  SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

         710         720         730         740         750
      *    *     *    *     *    *     *    *     *    *
  CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
  GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
   PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

         760         770         780         790         800
      *    *     *    *     *    *     *    *     *    *
  CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
  GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
 ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

         810         820         830         840         850
      *    *     *    *     *    *     *    *     *    *
  AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
  TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
  SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
```

FIG. 6C

```
       860       870       880       890       900
  *    *     *    *     *    *     *    *     *    *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
  ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

       910       920       930       940       950
  *    *     *    *     *    *     *    *     *    *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

       960       970       980       990      1000
  *    *     *    *     *    *     *    *     *    *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

      1010      1020      1030      1040      1050
  *    *     *    *     *    *     *    *     *    *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
 LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

      1060      1070      1080      1090      1100
  *    *     *    *     *    *     *    *     *    *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

      1110      1120      1130      1140      1150
  *    *     *    *     *    *     *    *     *    *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

      1160      1170      1180      1190      1200
  *    *     *    *     *    *     *    *     *    *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
 IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

      1210      1220      1230      1240      1250
  *    *     *    *     *    *     *    *     *    *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

      1260      1270      1280      1290      1300
  *    *     *    *     *    *     *    *     *    *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```

FIG. 6D

```
        1310       1320       1330       1340       1350
          *    *     *    *     *    *     *    *     *    *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
 ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

        1360       1370       1380
          *    *     *    *     *    *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)
```

FIG. 7A

Transcript 10
(Sequence Range: 1 to 1534)

```
        10         20         30         40         50
    *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                 MetGluTrpArg AsnLysLys>

        60         70         80         90        100
    *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

       110        120        130        140        150
    *    *     *    *     *    *     *    *     *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

       160        170        180        190        200
    *    *     *    *     *    *     *    *     *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

       210        220        230        240        250
    *    *     *    *     *    *     *    *     *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***(SEQ ID NO:11)

       260        270        280        290        300
    *    *     *    *     *    *     *    *     *    *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

       310        320        330        340        350
    *    *     *    *     *    *     *    *     *    *
TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

       360        370        380        390        400
    *    *     *    *     *    *     *    *     *    *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

FIG. 7B

```
       410         420         430         440         450
    *     *     *     *     *     *     *     *     *     *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

       460         470         480         490         500
    *     *     *     *     *     *     *     *     *     *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

       510         520         530         540         550
    *     *     *     *     *     *     *     *     *     *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

       560         570         580         590         600
    *     *     *     *     *     *     *     *     *     *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

       610         620         630         640         650
    *     *     *     *     *     *     *     *     *     *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

       660         670         680         690         700
    *     *     *     *     *     *     *     *     *     *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

       710         720         730         740         750
    *     *     *     *     *     *     *     *     *     *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

       760         770         780         790         800
    *     *     *     *     *     *     *     *     *     *
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

       810         820         830         840         850
    *     *     *     *     *     *     *     *     *     *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

       860         870         880         890         900
    *     *     *     *     *     *     *     *     *     *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

       910         920         930         940         950
    *     *     *     *     *     *     *     *     *     *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
```

FIG. 7C

```
       960        970        980        990       1000
    *    *     *    *     *    *     *    *     *    *
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

      1010       1020       1030       1040       1050
    *    *     *    *     *    *     *    *     *    *
TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

      1060       1070       1080       1090       1100
    *    *     *    *     *    *     *    *     *    *
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

      1110       1120       1130       1140       1150
    *    *     *    *     *    *     *    *     *    *
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

      1160       1170       1180       1190       1200
    *    *     *    *     *    *     *    *     *    *
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

      1210       1220       1230       1240       1250
    *    *     *    *     *    *     *    *     *    *
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

      1260       1270       1280       1290       1300
    *    *     *    *     *    *     *    *     *    *
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

      1310       1320       1330       1340       1350
    *    *     *    *     *    *     *    *     *    *
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

      1360       1370       1380       1390       1400
    *    *     *    *     *    *     *    *     *    *
CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

      1410       1420       1430       1440       1450
    *    *     *    *     *    *     *    *     *    *
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

      1460       1470       1480       1490       1500
    *    *     *    *     *    *     *    *     *    *
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

FIG. 7D

```
      1510       1520       1530
   *    *     *    *     *    *
TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)
```

FIG. 8A

```
         10         20         30         40         50
          *          *          *          *          *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

         60         70         80         90        100
          *          *          *          *          *
GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

        110        120        130        140        150
          *          *          *          *          *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

        160        170        180        190        200
          *          *          *          *          *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

        210        220        230        240        250
          *          *          *          *          *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

        260        270        280        290        300
          *          *          *          *          *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                            MetGluAla>

        310        320        330        340        350
          *          *          *          *          *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

        360        370        380        390        400
          *          *          *          *          *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

        410        420        430        440        450
          *          *          *          *          *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

        460        470        480        490        500
          *          *          *          *          *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
```

FIG. 8B

```
         510        520        530        540        550
           *          *          *          *          *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

         560        570        580        590        600
           *          *          *          *          *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
 GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

         610        620        630        640        650
           *          *          *          *          *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

         660        670        680        690        700
           *          *          *          *          *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

         710        720        730        740        750
           *          *          *          *          *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
 AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

         760        770        780        790        800
           *          *          *          *          *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

         810        820        830        840        850
           *          *          *          *          *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

         860        870        880        890        900
           *          *          *          *          *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
 AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

         910        920        930        940        950
           *          *          *          *          *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

         960        970        980        990       1000
           *          *          *          *          *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```

FIG. 8C

```
      1010       1020       1030       1040       1050
         *          *          *          *          *
CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
 IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

      1060       1070       1080       1090       1100
         *          *          *          *          *
TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

      1110       1120       1130       1140       1150
         *          *          *          *          *
ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

      1160       1170       1180       1190       1200
         *          *          *          *          *
CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
 CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

      1210       1220       1230       1240       1250
         *          *          *          *          *
GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

      1260       1270       1280       1290       1300
         *          *          *          *          *
AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

      1310       1320       1330       1340       1350
         *          *          *          *          *
CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
 IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

      1360       1370       1380       1390       1400
         *          *          *          *          *
CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

      1410       1420       1430       1440       1450
         *          *          *          *          *
CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

      1460       1470       1480       1490       1500
         *          *          *          *          *
AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
 AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

FIG. 8D

```
        1510       1520       1530       1540       1550
           *          *          *          *          *
 TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
 AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

        1560       1570
           *          *
 GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:7)
 CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:20)
 ValPheGly AsnGluIleSer ***> (SEQ ID NO:12)
```

Title: Isoforms of the Human Vitamin D Recept[or]
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FiG 1A.

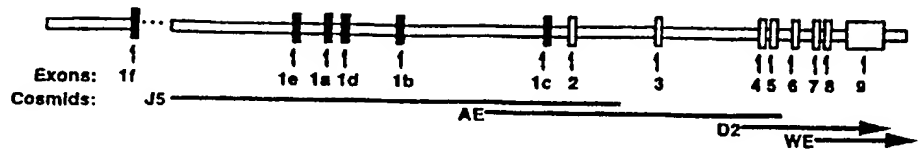

FiG 1B.

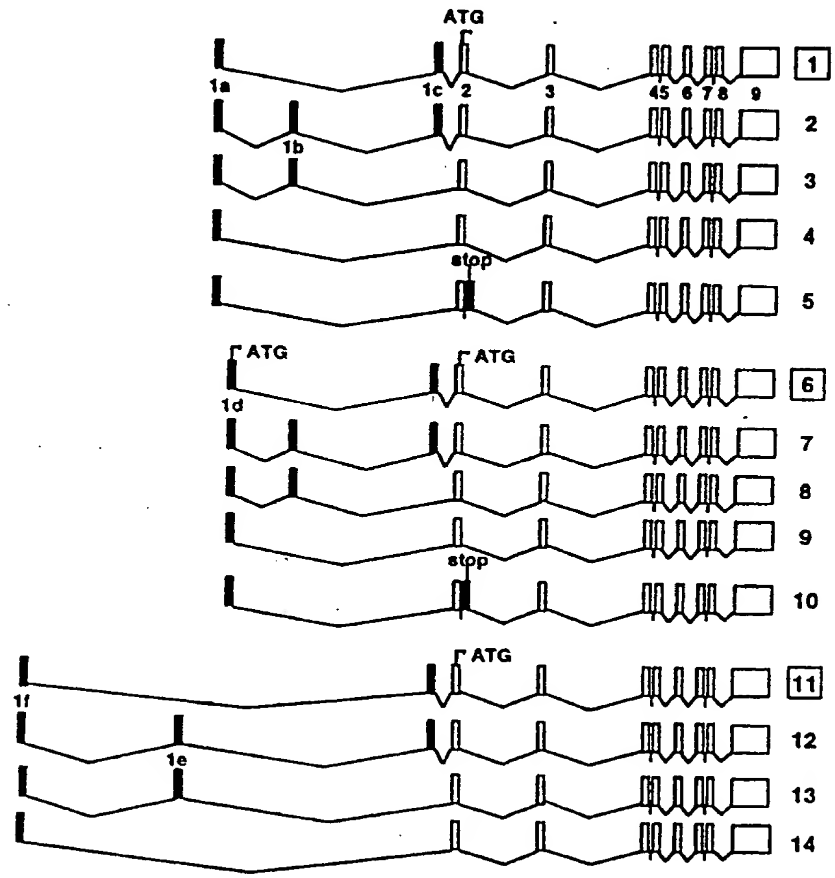

FiG 1C.

(SEQ ID NO:14)

Transcript 1: MEAMA ASTSL PDPGD FDRNV PRI DBD 427aa

Transcript 6: MEWRN KKRSD WLSMV LRTAG VEEAF GSEVS VRPHR RAPLG STYLP PAPSG MEAMA ASTSL PDPGD FDRNV PRI DBD 477aa (SEQ ID NO: 16)

Transcript 9: MEW RNKKR SDWLS MVLRT AGVEG MEAMA ASTSL PDPGD FDRNV PRI DBD 450aa

(SEQ ID NO: 15)

~~FIGURE 1~~

A. 5'...atcccttaag GGCTCCTGAACCTAGCCCAGCTGGACGGAG
AAATGGACTCTAGCCTCCTCTGATAGCCTCATGCCAGGCCC
CGTGCACATTGCTTTGCTTGCCTCCCTCAATCCTCATAGCT
TCTCTTTGGGgtaagtacag...3' (SEQ ID NO:13)

B. 5'...TGCGACCTTGGCGGTGAGCCTGGGGACAGGGGTGAGGC
CAGAGACGGACGGACGCAGGGGCCCGGCCCAAGGCGAGGG
AGAACAGCGGCACTAAGGCAGAAAGGAAGAGGGCGGTGTG
TTCACCCGCAGCCCAATCCATCACTCAGCAACTCCTAGAC
GCTGGTAGAAAGTTCCTCCGAGGAGCCTGCCATCCAGTCGT
GCGTGCAG...3' (SEQ ID NO: 5)

C. 5'...tgtttttag AGGCAGCATGAAACAGTGGGATGTGCAGAG
AGAAGATCTGGGTCCAGTAGCTCTGACACTCCTCAGCTGT
AGAAACCTTGACAACTCTGCACATCAGTTGTACAATGGAA
CGGTATTTTTTACTCTTCATGTCTGAAAAGGCTATGATAA
AGATCAAgtaagatatt...3' (SEQ ID NO:6)

D. 5'...GTTTCCTTCTTCTGTCGGGGCGCCTTGGC$\boxed{\text{ATG}}$GAGTGG
AGGAATAAGAAAAGGAGCGATTGGCTGTCG$\boxed{\text{ATG}}$GTGCTCA
GAACTGCTGGAGTGGAGGgtgtgtaacc...3' (SEQ ID NO: 1)

FIG. 4
~~FIGURE 4~~

FIG. 5A
~~FIGURE 5~~ TRANSCRIPT 6

(Sequence Range: 1 to 1463)

```
         10         20         30         40         50
     *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                MetGluTrpArg AsnLysLys>

         60         70         80         90        100
     *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGAAGC
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCTTCG
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGluAla>

        110        120        130        140        150
     *    *     *    *     *    *     *    *     *    *
CTTTGGGTCT GAAGTGTCTG TGAGACCTCA CAGAAGAGCA CCCCTGGGCT
GAAACCCAGA CTTCACAGAC ACTCTGGAGT GTCTTCTCGT GGGGACCCGA
 PheGlySer GluValSer ValArgProHis ArgArgAla ProLeuGly>

        160        170        180        190        200
     *    *     *    *     *    *     *    *     *    *
CCACTTACCT GCCCCCTGCT CCTTCAGGGA TGGAGGCAAT GGCGGCCAGC
GGTGAATGGA CGGGGGACGA GGAAGTCCCT ACCTCCGTTA CCGCCGGTCG
SerThrTyrLeu ProProAla ProSerGly MetGluAlaMet AlaAlaSer>

        210        220        230        240        250
     *    *     *    *     *    *     *    *     *    *
ACTTCCCTGC CTGACCCTGG AGACTTTGAC CGGAACGTGC CCCGGATCTG
TGAAGGGACG GACTGGGACC TCTGAAACTG GCCTTGCACG GGGCCTAGAC
ThrSerLeu ProAspProGly AspPheAsp ArgAsnVal ProArgIleCys>

        260        270        280        290        300
     *    *     *    *     *    *     *    *     *    *
TGGGGTGTGT GGAGACCGAG CCACTGGCTT TCACTTCAAT GCTATGACCT
ACCCCACACA CCTCTGGCTC GGTGACCGAA AGTGAAGTTA CGATACTGGA
 GlyValCys GlyAspArg AlaThrGlyPhe HisPheAsn AlaMetThr>

        310        320        330        340        350
     *    *     *    *     *    *     *    *     *    *
GTGAAGGCTG CAAAGGCTTC TTCAGGCGAA GCATGAAGCG GAAGGCACTA
CACTTCCGAC GTTTCCGAAG AAGTCCGCTT CGTACTTCGC CTTCCGTGAT
CysGluGlyCys LysGlyPhe PheArgArg SerMetLysArg LysAlaLeu>

        360        370        380        390        400
     *    *     *    *     *    *     *    *     *    *
TTCACCTGCC CCTTCAACGG GGACTGCCGC ATCACCAAGG ACAACCGACG
AAGTGGACGG GGAAGTTGCC CCTGACGGCG TAGTGGTTCC TGTTGGCTGC
PheThrCys ProPheAsnGly AspCysArg IleThrLys AspAsnArgArg>
```

FIG 5B


```
       410         420         430         440         450
        *    *      *    *      *    *      *    *      *    *
 CCACTGCCAG GCCTGCCGGC TCAAACGCTG TGTGGACATC GGCATGATGA
 GGTGACGGTC CGGACGGCCG AGTTTGCGAC ACACCTGTAG CCGTACTACT
  HisCysGln AlaCysArg LeuLysArgCys ValAspIle GlyMetMet>

       460         470         480         490         500
        *    *      *    *      *    *      *    *      *    *
 AGGAGTTCAT TCTGACAGAT GAGGAAGTGC AGAGGAAGCG GGAGATGATC
 TCCTCAAGTA AGACTGTCTA CTCCTTCACG TCTCCTTCGC CCTCTACTAG
LysGluPheIle LeuThrAsp GluGluVal GlnArgLysArg GluMetIle>

       510         520         530         540         550
        *    *      *    *      *    *      *    *      *    *
 CTGAAGCGGA AGGAGGAGGA GGCCTTGAAG GACAGTCTGC GGCCCAAGCT
 GACTTCGCCT TCCTCCTCCT CCGGAACTTC CTGTCAGACG CCGGGTTCGA
 LeuLysArg LysGluGluGlu AlaLeuLys AspSerLeu ArgProLysLeu>

       560         570         580         590         600
        *    *      *    *      *    *      *    *      *    *
 GTCTGAGGAG CAGCAGCGCA TCATTGCCAT ACTGCTGGAC GCCCACCATA
 CAGACTCCTC GTCGTCGCGT AGTAACGGTA TGACGACCTG CGGGTGGTAT
  SerGluGlu GlnGlnArg IleIleAlaIle LeuLeuAsp AlaHisHis>

       610         620         630         640         650
        *    *      *    *      *    *      *    *      *    *
 AGACCTACGA CCCCACCTAC TCCGACTTCT GCCAGTTCCG GCCTCCAGTT
 TCTGGATGCT GGGGTGGATG AGGCTGAAGA CGGTCAAGGC CGGAGGTCAA
LysThrTyrAsp ProThrTyr SerAspPhe CysGlnPheArg ProProVal>

       660         670         680         690         700
        *    *      *    *      *    *      *    *      *    *
 CGTGTGAATG ATGGTGGAGG GAGCCATCCT TCCAGGCCCA ACTCCAGACA
 GCACACTTAC TACCACCTCC CTCGGTAGGA AGGTCCGGGT TGAGGTCTGT
 ArgValAsn AspGlyGlyGly SerHisPro SerArgPro AsnSerArgHis>

       710         720         730         740         750
        *    *      *    *      *    *      *    *      *    *
 CACTCCCAGC TTCTCTGGGG ACTCCTCCTC CTCCTGCTCA GATCACTGTA
 GTGAGGGTCG AAGAGACCCC TGAGGAGGAG GAGGACGAGT CTAGTGACAT
  ThrProSer PheSerGly AspSerSerSer SerCysSer AspHisCys>

       760         770         780         790         800
        *    *      *    *      *    *      *    *      *    *
 TCACCTCTTC AGACATGATG GACTCGTCCA GCTTCTCCAA TCTGGATCTG
 AGTGGAGAAG TCTGTACTAC CTGAGCAGGT CGAAGAGGTT AGACCTAGAC
IleThrSerSer AspMetMet AspSerSer SerPheSerAsn LeuAspLeu>

       810         820         830         840         850
        *    *      *    *      *    *      *    *      *    *
 AGTGAAGAAG ATTCAGATGA CCCTTCTGTG ACCCTAGAGC TGTCCCAGCT
 TCACTTCTTC TAAGTCTACT GGGAAGACAC TGGGATCTCG ACAGGGTCGA
 SerGluGlu AspSerAspAsp ProSerVal ThrLeuGlu LeuSerGlnLeu>
```

FIG 5C


```
       860       870       880       890       900
  *    *    *    *    *    *    *    *    *    *
CTCCATGCTG CCCCACCTGG CTGACCTGGT CAGTTACAGC ATCCAAAAGG
GAGGTACGAC GGGGTGGACC GACTGGACCA GTCAATGTCG TAGGTTTTCC
 SerMetLeu ProHisLeu AlaAspLeuVal SerTyrSer IleGlnLys>

       910       920       930       940       950
  *    *    *    *    *    *    *    *    *    *
TCATTGGCTT TGCTAAGATG ATACCAGGAT TCAGAGACCT CACCTCTGAG
AGTAACCGAA ACGATTCTAC TATGGTCCTA AGTCTCTGGA GTGGAGACTC
ValIleGlyPhe AlaLysMet IleProGly PheArgAspLeu ThrSerGlu>

       960       970       980       990      1000
  *    *    *    *    *    *    *    *    *    *
GACCAGATCG TACTGCTGAA GTCAAGTGCC ATTGAGGTCA TCATGTTGCG
CTGGTCTAGC ATGACGACTT CAGTTCACGG TAACTCCAGT AGTACAACGC
AspGlnIle ValLeuLeuLys SerSerAla IleGluVal IleMetLeuArg>

      1010      1020      1030      1040      1050
  *    *    *    *    *    *    *    *    *    *
CTCCAATGAG TCCTTCACCA TGGACGACAT GTCCTGGACC TGTGGCAACC
GAGGTTACTC AGGAAGTGGT ACCTGCTGTA CAGGACCTGG ACACCGTTGG
 SerAsnGlu SerPheThr MetAspAspMet SerTrpThr CysGlyAsn>

      1060      1070      1080      1090      1100
  *    *    *    *    *    *    *    *    *    *
AAGACTACAA GTACCGCGTC AGTGACGTGA CCAAAGCCGG ACACAGCCTG
TTCTGATGTT CATGGCGCAG TCACTGCACT GGTTTCGGCC TGTGTCGGAC
GlnAspTyrLys TyrArgVal SerAspVal ThrLysAlaGly HisSerLeu>

      1110      1120      1130      1140      1150
  *    *    *    *    *    *    *    *    *    *
GAGCTGATTG AGCCCCTCAT CAAGTTCCAG GTGGGACTGA AGAAGCTGAA
CTCGACTAAC TCGGGGAGTA GTTCAAGGTC CACCCTGACT TCTTCGACTT
GluLeuIle GluProLeuIle LysPheGln ValGlyLeu LysLysLeuAsn>

      1160      1170      1180      1190      1200
  *    *    *    *    *    *    *    *    *    *
CTTGCATGAG GAGGAGCATG TCCTGCTCAT GGCCATCTGC ATCGTCTCCC
GAACGTACTC CTCCTCGTAC AGGACGAGTA CCGGTAGACG TAGCAGAGGG
 LeuHisGlu GluGluHis ValLeuLeuMet AlaIleCys IleValSer>

      1210      1220      1230      1240      1250
  *    *    *    *    *    *    *    *    *    *
CAGATCGTCC TGGGGTGCAG GACGCCGCGC TGATTGAGGC CATCCAGGAC
GTCTAGCAGG ACCCCACGTC CTGCGGCGCG ACTAACTCCG GTAGGTCCTG
ProAspArgPro GlyValGln AspAlaAla LeuIleGluAla IleGlnAsp>

      1260      1270      1280      1290      1300
  *    *    *    *    *    *    *    *    *    *
CGCCTGTCCA ACACACTGCA GACGTACATC CGCTGCCGCC ACCCGCCCCC
GCGGACAGGT TGTGTGACGT CTGCATGTAG GCGACGGCGG TGGGCGGGGG
ArgLeuSer AsnThrLeuGln ThrTyrIle ArgCysArg HisProProPro>
```

FIG 5D

~~8/20~~

```
          1310        1320        1330        1340        1350
       *     *     *     *     *     *     *     *     *     *
GGGCAGCCAC CTGCTCTATG CCAAGATGAT CCAGAAGCTA GCCGACCTGC
CCCGTCGGTG GACGAGATAC GGTTCTACTA GGTCTTCGAT CGGCTGGACG
 GlySerHis LeuLeuTyr AlaLysMetIle GlnLysLeu AlaAspLeu>

          1360        1370        1380        1390        1400
       *     *     *     *     *     *     *     *     *     *
GCAGCCTCAA TGAGGAGCAC TCCAAGCAGT ACCGCTGCCT CTCCTTCCAG
CGTCGGAGTT ACTCCTCGTG AGGTTCGTCA TGGCGACGGA GAGGAAGGTC
ArgSerLeuAsn GluGluHis SerLysGln TyrArgCysLeu SerPheGln>

          1410        1420        1430        1440        1450
       *     *     *     *     *     *     *     *     *     *
CCTGAGTGCA GCATGAAGCT AACGCCCCTT GTGCTCGAAG TGTTTGGCAA
GGACTCACGT CGTACTTCGA TTGCGGGGAA CACGAGCTTC ACAAACCGTT
ProGluCys SerMetLysLeu ThrProLeu ValLeuGlu ValPheGlyAsn>

          1460
       *     *
TGAGATCTCC TGA (SEQ ID NO: 2)
ACTCTAGAGG ACT (SEQ ID NO: 17)
 GluIleSer ***> (SEQ ID NO: 9)
```

~~WO 99/46872~~ ~~PCT/AU98/00817~~

~~9/20~~

FIG. 6A

~~FIGURE 6~~ TRANSCRIPT 9

(Sequence Range: 1 to 1382)

```
          10         20         30         40         50
     *    *    *    *    *    *    *    *    *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                MetGluTrpArg AsnLysLys>

          60         70         80         90        100
     *    *    *    *    *    *    *    *    *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

         110        120        130        140        150
     *    *    *    *    *    *    *    *    *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

         160        170        180        190        200
     *    *    *    *    *    *    *    *    *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

         210        220        230        240        250
     *    *    *    *    *    *    *    *    *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGCGAAG
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCGCTTC
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArgArgSer>

         260        270        280        290        300
     *    *    *    *    *    *    *    *    *    *
CATGAAGCGG AAGGCACTAT TCACCTGCCC CTTCAACGGG GACTGCCGCA
GTACTTCGCC TTCCGTGATA AGTGGACGGG GAAGTTGCCC CTGACGGCGT
 MetLysArg LysAlaLeu PheThrCysPro PheAsnGly AspCysArg>

         310        320        330        340        350
     *    *    *    *    *    *    *    *    *    *
TCACCAAGGA CAACCGACGC CACTGCCAGG CCTGCCGGCT CAAACGCTGT
AGTGGTTCCT GTTGGCTGCG GTGACGGTCC GGACGGCCGA GTTTGCGACA
IleThrLysAsp AsnArgArg HisCysGln AlaCysArgLeu LysArgCys>

         360        370        380        390        400
     *    *    *    *    *    *    *    *    *    *
GTGGACATCG GCATGATGAA GGAGTTCATT CTGACAGATG AGGAAGTGCA
CACCTGTAGC CGTACTACTT CCTCAAGTAA GACTGTCTAC TCCTTCACGT
ValAspIle GlyMetMetLys GluPheIle LeuThrAsp GluGluValGln>
```

FIG 6B

~~10/20~~

```
        410        420        430        440        450
     *    *    *    *    *    *    *    *    *    *
GAGGAAGCGG GAGATGATCC TGAAGCGGAA GGAGGAGGAG GCCTTGAAGG
CTCCTTCGCC CTCTACTAGG ACTTCGCCTT CCTCCTCCTC CGGAACTTCC
 ArgLysArg GluMetIle LeuLysArgLys GluGluGlu AlaLeuLys>

        460        470        480        490        500
     *    *    *    *    *    *    *    *    *    *
ACAGTCTGCG GCCCAAGCTG TCTGAGGAGC AGCAGCGCAT CATTGCCATA
TGTCAGACGC CGGGTTCGAC AGACTCCTCG TCGTCGCGTA GTAACGGTAT
AspSerLeuArg ProLysLeu SerGluGlu GlnGlnArgIle IleAlaIle>

        510        520        530        540        550
     *    *    *    *    *    *    *    *    *    *
CTGCTGGACG CCCACCATAA GACCTACGAC CCCACCTACT CCGACTTCTG
GACGACCTGC GGGTGGTATT CTGGATGCTG GGGTGGATGA GGCTGAAGAC
LeuLeuAsp AlaHisHisLys ThrTyrAsp ProThrTyr SerAspPheCys>

        560        570        580        590        600
     *    *    *    *    *    *    *    *    *    *
CCAGTTCCGG CCTCCAGTTC GTGTGAATGA TGGTGGAGGG AGCCATCCTT
GGTCAAGGCC GGAGGTCAAG CACACTTACT ACCACCTCCC TCGGTAGGAA
 GlnPheArg ProProVal ArgValAsnAsp GlyGlyGly SerHisPro>

        610        620        630        640        650
     *    *    *    *    *    *    *    *    *    *
CCAGGCCCAA CTCCAGACAC ACTCCCAGCT TCTCTGGGGA CTCCTCCTCC
GGTCCGGGTT GAGGTCTGTG TGAGGGTCGA AGAGACCCCT GAGGAGGAGG
SerArgProAsn SerArgHis ThrProSer PheSerGlyAsp SerSerSer>

        660        670        680        690        700
     *    *    *    *    *    *    *    *    *    *
TCCTGCTCAG ATCACTGTAT CACCTCTTCA GACATGATGG ACTCGTCCAG
AGGACGAGTC TAGTGACATA GTGGAGAAGT CTGTACTACC TGAGCAGGTC
SerCysSer AspHisCysIle ThrSerSer AspMetMet AspSerSerSer>

        710        720        730        740        750
     *    *    *    *    *    *    *    *    *    *
CTTCTCCAAT CTGGATCTGA GTGAAGAAGA TTCAGATGAC CCTTCTGTGA
GAAGAGGTTA GACCTAGACT CACTTCTTCT AAGTCTACTG GGAAGACACT
 PheSerAsn LeuAspLeu SerGluGluAsp SerAspAsp ProSerVal>

        760        770        780        790        800
     *    *    *    *    *    *    *    *    *    *
CCCTAGAGCT GTCCCAGCTC TCCATGCTGC CCCACCTGGC TGACCTGGTC
GGGATCTCGA CAGGGTCGAG AGGTACGACG GGGTGGACCG ACTGGACCAG
ThrLeuGluLeu SerGlnLeu SerMetLeu ProHisLeuAla AspLeuVal>

        810        820        830        840        850
     *    *    *    *    *    *    *    *    *    *
AGTTACAGCA TCCAAAAGGT CATTGGCTTT GCTAAGATGA TACCAGGATT
TCAATGTCGT AGGTTTTCCA GTAACCGAAA CGATTCTACT ATGGTCCTAA
SerTyrSer IleGlnLysVal IleGlyPhe AlaLysMet IleProGlyPhe>
```

FIG 6C

1 ~~11/20~~

```
       860        870        880        890        900
         *    *     *    *     *    *     *    *     *    *
CAGAGACCTC ACCTCTGAGG ACCAGATCGT ACTGCTGAAG TCAAGTGCCA
GTCTCTGGAG TGGAGACTCC TGGTCTAGCA TGACGACTTC AGTTCACGGT
 ArgAspLeu ThrSerGlu AspGlnIleVal LeuLeuLys SerSerAla>

       910        920        930        940        950
         *    *     *    *     *    *     *    *     *    *
TTGAGGTCAT CATGTTGCGC TCCAATGAGT CCTTCACCAT GGACGACATG
AACTCCAGTA GTACAACGCG AGGTTACTCA GGAAGTGGTA CCTGCTGTAC
IleGluValIle MetLeuArg SerAsnGlu SerPheThrMet AspAspMet>

       960        970        980        990       1000
         *    *     *    *     *    *     *    *     *    *
TCCTGGACCT GTGGCAACCA AGACTACAAG TACCGCGTCA GTGACGTGAC
AGGACCTGGA CACCGTTGGT TCTGATGTTC ATGGCGCAGT CACTGCACTG
SerTrpThr CysGlyAsnGln AspTyrLys TyrArgVal SerAspValThr>

      1010       1020       1030       1040       1050
         *    *     *    *     *    *     *    *     *    *
CAAAGCCGGA CACAGCCTGG AGCTGATTGA GCCCCTCATC AAGTTCCAGG
GTTTCGGCCT GTGTCGGACC TCGACTAACT CGGGGAGTAG TTCAAGGTCC
 LysAlaGly HisSerLeu GluLeuIleGlu ProLeuIle LysPheGln>

      1060       1070       1080       1090       1100
         *    *     *    *     *    *     *    *     *    *
TGGGACTGAA GAAGCTGAAC TTGCATGAGG AGGAGCATGT CCTGCTCATG
ACCCTGACTT CTTCGACTTG AACGTACTCC TCCTCGTACA GGACGAGTAC
ValGlyLeuLys LysLeuAsn LeuHisGlu GluGluHisVal LeuLeuMet>

      1110       1120       1130       1140       1150
         *    *     *    *     *    *     *    *     *    *
GCCATCTGCA TCGTCTCCCC AGATCGTCCT GGGGTGCAGG ACGCCGCGCT
CGGTAGACGT AGCAGAGGGG TCTAGCAGGA CCCCACGTCC TGCGGCGCGA
AlaIleCys IleValSerPro AspArgPro GlyValGln AspAlaAlaLeu>

      1160       1170       1180       1190       1200
         *    *     *    *     *    *     *    *     *    *
GATTGAGGCC ATCCAGGACC GCCTGTCCAA CACACTGCAG ACGTACATCC
CTAACTCCGG TAGGTCCTGG CGGACAGGTT GTGTGACGTC TGCATGTAGG
 IleGluAla IleGlnAsp ArgLeuSerAsn ThrLeuGln ThrTyrIle>

      1210       1220       1230       1240       1250
         *    *     *    *     *    *     *    *     *    *
GCTGCCGCCA CCCGCCCCCG GGCAGCCACC TGCTCTATGC CAAGATGATC
CGACGGCGGT GGGCGGGGGC CCGTCGGTGG ACGAGATACG GTTCTACTAG
ArgCysArgHis ProProPro GlySerHis LeuLeuTyrAla LysMetIle>

      1260       1270       1280       1290       1300
         *    *     *    *     *    *     *    *     *    *
CAGAAGCTAG CCGACCTGCG CAGCCTCAAT GAGGAGCACT CCAAGCAGTA
GTCTTCGATC GGCTGGACGC GTCGGAGTTA CTCCTCGTGA GGTTCGTCAT
GlnLysLeu AlaAspLeuArg SerLeuAsn GluGluHis SerLysGlnTyr>
```

FIG 6D ~~12/20~~

```
            1310        1320        1330        1340        1350
               *    *      *    *      *    *     *    *      *    *
CCGCTGCCTC TCCTTCCAGC CTGAGTGCAG CATGAAGCTA ACGCCCCTTG
GGCGACGGAG AGGAAGGTCG GACTCACGTC GTACTTCGAT TGCGGGGAAC
 ArgCysLeu SerPheGln ProGluCysSer MetLysLeu ThrProLeu>

            1360        1370        1380
               *    *      *    *      *    *
TGCTCGAAGT GTTTGGCAAT GAGATCTCCT GA (SEQ ID NO:3)
ACGAGCTTCA CAAACCGTTA CTCTAGAGGA CT (SEQ ID NO:18)
ValLeuGluVal PheGlyAsn GluIleSer ***> (SEQ ID NO:10)
```

FIG 7A

~~FIGURE 7~~ TRANSCRIPT 10

(Sequence Range: 1 to 1534)

```
        10         20         30         40         50
    *    *     *    *     *    *     *    *     *    *
GTTTCCTTCT TCTGTCGGGG CGCCTTGGCA TGGAGTGGAG GAATAAGAAA
CAAAGGAAGA AGACAGCCCC GCGGAACCGT ACCTCACCTC CTTATTCTTT
                                 MetGluTrpArg AsnLysLys>

        60         70         80         90        100
    *    *     *    *     *    *     *    *     *    *
AGGAGCGATT GGCTGTCGAT GGTGCTCAGA ACTGCTGGAG TGGAGGGGAT
TCCTCGCTAA CCGACAGCTA CCACGAGTCT TGACGACCTC ACCTCCCCTA
ArgSerAsp TrpLeuSerMet ValLeuArg ThrAlaGly ValGluGlyMet>

       110        120        130        140        150
    *    *     *    *     *    *     *    *     *    *
GGAGGCAATG GCGGCCAGCA CTTCCCTGCC TGACCCTGGA GACTTTGACC
CCTCCGTTAC CGCCGGTCGT GAAGGGACGG ACTGGGACCT CTGAAACTGG
 GluAlaMet AlaAlaSer ThrSerLeuPro AspProGly AspPheAsp>

       160        170        180        190        200
    *    *     *    *     *    *     *    *     *    *
GGAACGTGCC CCGGATCTGT GGGGTGTGTG GAGACCGAGC CACTGGCTTT
CCTTGCACGG GGCCTAGACA CCCCACACAC CTCTGGCTCG GTGACCGAAA
ArgAsnValPro ArgIleCys GlyValCys GlyAspArgAla ThrGlyPhe>

       210        220        230        240        250
    *    *     *    *     *    *     *    *     *    *
CACTTCAATG CTATGACCTG TGAAGGCTGC AAAGGCTTCT TCAGGTGAGC
GTGAAGTTAC GATACTGGAC ACTTCCGACG TTTCCGAAGA AGTCCACTCG
HisPheAsn AlaMetThrCys GluGlyCys LysGlyPhe PheArg***

       260        270        280        290        300
    *    *     *    *     *    *     *    *     *    *
CCCCCTCCCA GGCTCTCCCC AGTGGAAAGG GAGGGAGAAG AAGCAAGGTG
GGGGGAGGGT CCGAGAGGGG TCACCTTTCC CTCCCTCTTC TTCGTTCCAC

       310        320        330        340        350
    *    *     *    *     *    *     *    *     *    *
TTTCCATGAA GGGAGCCCTT GCATTTTTCA CATCTCCTTC CTTACAATGT
AAAGGTACTT CCCTCGGGAA CGTAAAAAGT GTAGAGGAAG GAATGTTACA

       360        370        380        390        400
    *    *     *    *     *    *     *    *     *    *
CCATGGAACA TGCGGCGCTC ACAGCCACAG GAGCAGGAGG GTCTTGGCGA
GGTACCTTGT ACGCCGCGAG TGTCGGTGTC CTCGTCCTCC CAGAACCGCT
```

FIG 7B


```
       410        420        430        440        450
   *    *    *    *    *    *    *    *    *    *
AGCATGAAGC GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG
TCGTACTTCG CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC

       460        470        480        490        500
   *    *    *    *    *    *    *    *    *    *
CATCACCAAG GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT
GTAGTGGTTC CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA

       510        520        530        540        550
   *    *    *    *    *    *    *    *    *    *
GTGTGGACAT CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG
CACACCTGTA GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC

       560        570        580        590        600
   *    *    *    *    *    *    *    *    *    *
CAGAGGAAGC GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA
GTCTCCTTCG CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT

       610        620        630        640        650
   *    *    *    *    *    *    *    *    *    *
GGACAGTCTG CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA
CCTGTCAGAC GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT

       660        670        680        690        700
   *    *    *    *    *    *    *    *    *    *
TACTGCTGGA CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC
ATGACGACCT GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG

       710        720        730        740        750
   *    *    *    *    *    *    *    *    *    *
TGCCAGTTCC GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC
ACGGTCAAGG CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG

       760        770        780        790        800
   *    *    *    *    *    *    *    *    *    *
TTCCAGGCCC AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT
AAGGTCCGGG TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA

       810        820        830        840        850
   *    *    *    *    *    *    *    *    *    *
CCTCCTGCTC AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC
GGAGGACGAG TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG

       860        870        880        890        900
   *    *    *    *    *    *    *    *    *    *
AGCTTCTCCA ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT
TCGAAGAGGT TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA

       910        920        930        940        950
   *    *    *    *    *    *    *    *    *    *
GACCCTAGAG CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG
CTGGGATCTC GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC
```

FIG 7C


```
       960        970        980        990       1000
     *    *     *    *     *    *     *    *     *    *
TCAGTTACAG CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA
AGTCAATGTC GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT

      1010       1020       1030       1040       1050
     *    *     *    *     *    *     *    *     *    *
TTCAGAGACC TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC
AAGTCTCTGG AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG

      1060       1070       1080       1090       1100
     *    *     *    *     *    *     *    *     *    *
CATTGAGGTC ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA
GTAACTCCAG TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT

      1110       1120       1130       1140       1150
     *    *     *    *     *    *     *    *     *    *
TGTCCTGGAC CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG
ACAGGACCTG GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC

      1160       1170       1180       1190       1200
     *    *     *    *     *    *     *    *     *    *
ACCAAAGCCG GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA
TGGTTTCGGC CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT

      1210       1220       1230       1240       1250
     *    *     *    *     *    *     *    *     *    *
GGTGGGACTG AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA
CCACCCTGAC TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT

      1260       1270       1280       1290       1300
     *    *     *    *     *    *     *    *     *    *
TGGCCATCTG CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG
ACCGGTAGAC GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC

      1310       1320       1330       1340       1350
     *    *     *    *     *    *     *    *     *    *
CTGATTGAGG CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT
GACTAACTCC GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA

      1360       1370       1380       1390       1400
     *    *     *    *     *    *     *    *     *    *
CCGCTGCCGC CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA
GGCGACGGCG GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT

      1410       1420       1430       1440       1450
     *    *     *    *     *    *     *    *     *    *
TCCAGAAGCT AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG
AGGTCTTCGA TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC

      1460       1470       1480       1490       1500
     *    *     *    *     *    *     *    *     *    *
TACCGCTGCC TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT
ATGGCGACGG AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA
```

FIG 7D ~~16/20~~

```
      1510        1520        1530
   *      *     *      *     *      *
TGTGCTCGAA GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO:4)
ACACGAGCTT CACAAACCGT TACTCTAGAG GACT (SEQ ID NO:19)
```

Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG 8A

~~FIGURE 8~~ TRANSCRIPT 11

```
        10         20         30         40         50
         *          *          *          *          *
TGCGACCTTG GCGGTGAGCC TGGGGACAGG GGTGAGGCCA GAGACGGACG
ACGCTGGAAC CGCCACTCGG ACCCCTGTCC CCACTCCGGT CTCTGCCTGC

        60         70         80         90        100
         *          *          *          *          *
GACGCAGGGG CCCGGCCCAA GGCGAGGGAG AACAGCGGCA CTAAGGCAGA
CTGCGTCCCC GGGCCGGGTT CCGCTCCCTC TTGTCGCCGT GATTCCGTCT

       110        120        130        140        150
         *          *          *          *          *
AAGGAAGAGG GCGGTGTGTT CACCCGCAGC CCAATCCATC ACTCAGCAAC
TTCCTTCTCC CGCCACACAA GTGGGCGTCG GGTTAGGTAG TGAGTCGTTG

       160        170        180        190        200
         *          *          *          *          *
TCCTAGACGC TGGTAGAAAG TTCCTCCGAG GAGCCTGCCA TCCAGTCGTG
AGGATCTGCG ACCATCTTTC AAGGAGGCTC CTCGGACGGT AGGTCAGCAC

       210        220        230        240        250
         *          *          *          *          *
CGTGCAGAAG CCTTTGGGTC TGAAGTGTCT GTGAGACCTC ACAGAAGAGC
GCACGTCTTC GGAAACCCAG ACTTCACAGA CACTCTGGAG TGTCTTCTCG

       260        270        280        290        300
         *          *          *          *          *
ACCCCTGGGC TCCACTTACC TGCCCCCTGC TCCTTCAGGG ATGGAGGCAA
TGGGGACCCG AGGTGAATGG ACGGGGGACG AGGAAGTCCC TACCTCCGTT
                                            MetGluAla>

       310        320        330        340        350
         *          *          *          *          *
TGGCGGCCAG CACTTCCCTG CCTGACCCTG GAGACTTTGA CCGGAACGTG
ACCGCCGGTC GTGAAGGGAC GGACTGGGAC CTCTGAAACT GGCCTTGCAC
MetAlaAlaSer ThrSerLeu ProAspPro GlyAspPheAsp ArgAsnVal>

       360        370        380        390        400
         *          *          *          *          *
CCCCGGATCT GTGGGGTGTG TGGAGACCGA GCCACTGGCT TTCACTTCAA
GGGGCCTAGA CACCCCACAC ACCTCTGGCT CGGTGACCGA AAGTGAAGTT
ProArgIle CysGlyValCys GlyAspArg AlaThrGly PheHisPheAsn>

       410        420        430        440        450
         *          *          *          *          *
TGCTATGACC TGTGAAGGCT GCAAAGGCTT CTTCAGGCGA AGCATGAAGC
ACGATACTGG ACACTTCCGA CGTTTCCGAA GAAGTCCGCT TCGTACTTCG
 AlaMetThr CysGluGly CysLysGlyPhe PheArgArg SerMetLys>

       460        470        480        490        500
         *          *          *          *          *
GGAAGGCACT ATTCACCTGC CCCTTCAACG GGGACTGCCG CATCACCAAG
CCTTCCGTGA TAAGTGGACG GGGAAGTTGC CCCTGACGGC GTAGTGGTTC
ArgLysAlaLeu PheThrCys ProPheAsn GlyAspCysArg IleThrLys>
```

FIG 8B


```
       510        520        530        540        550
         *          *          *          *          *
GACAACCGAC GCCACTGCCA GGCCTGCCGG CTCAAACGCT GTGTGGACAT
CTGTTGGCTG CGGTGACGGT CCGGACGGCC GAGTTTGCGA CACACCTGTA
AspAsnArg ArgHisCysGln AlaCysArg LeuLysArg CysValAspIle>

       560        570        580        590        600
         *          *          *          *          *
CGGCATGATG AAGGAGTTCA TTCTGACAGA TGAGGAAGTG CAGAGGAAGC
GCCGTACTAC TTCCTCAAGT AAGACTGTCT ACTCCTTCAC GTCTCCTTCG
 GlyMetMet LysGluPhe IleLeuThrAsp GluGluVal GlnArgLys>

       610        620        630        640        650
         *          *          *          *          *
GGGAGATGAT CCTGAAGCGG AAGGAGGAGG AGGCCTTGAA GGACAGTCTG
CCCTCTACTA GGACTTCGCC TTCCTCCTCC TCCGGAACTT CCTGTCAGAC
ArgGluMetIle LeuLysArg LysGluGlu GluAlaLeuLys AspSerLeu>

       660        670        680        690        700
         *          *          *          *          *
CGGCCCAAGC TGTCTGAGGA GCAGCAGCGC ATCATTGCCA TACTGCTGGA
GCCGGGTTCG ACAGACTCCT CGTCGTCGCG TAGTAACGGT ATGACGACCT
ArgProLys LeuSerGluGlu GlnGlnArg IleIleAla IleLeuLeuAsp>

       710        720        730        740        750
         *          *          *          *          *
CGCCCACCAT AAGACCTACG ACCCCACCTA CTCCGACTTC TGCCAGTTCC
GCGGGTGGTA TTCTGGATGC TGGGGTGGAT GAGGCTGAAG ACGGTCAAGG
 AlaHisHis LysThrTyr AspProThrTyr SerAspPhe CysGlnPhe>

       760        770        780        790        800
         *          *          *          *          *
GGCCTCCAGT TCGTGTGAAT GATGGTGGAG GGAGCCATCC TTCCAGGCCC
CCGGAGGTCA AGCACACTTA CTACCACCTC CCTCGGTAGG AAGGTCCGGG
ArgProProVal ArgValAsn AspGlyGly GlySerHisPro SerArgPro>

       810        820        830        840        850
         *          *          *          *          *
AACTCCAGAC ACACTCCCAG CTTCTCTGGG GACTCCTCCT CCTCCTGCTC
TTGAGGTCTG TGTGAGGGTC GAAGAGACCC CTGAGGAGGA GGAGGACGAG
AsnSerArg HisThrProSer PheSerGly AspSerSer SerSerCysSer>

       860        870        880        890        900
         *          *          *          *          *
AGATCACTGT ATCACCTCTT CAGACATGAT GGACTCGTCC AGCTTCTCCA
TCTAGTGACA TAGTGGAGAA GTCTGTACTA CCTGAGCAGG TCGAAGAGGT
 AspHisCys IleThrSer SerAspMetMet AspSerSer SerPheSer>

       910        920        930        940        950
         *          *          *          *          *
ATCTGGATCT GAGTGAAGAA GATTCAGATG ACCCTTCTGT GACCCTAGAG
TAGACCTAGA CTCACTTCTT CTAAGTCTAC TGGGAAGACA CTGGGATCTC
AsnLeuAspLeu SerGluGlu AspSerAsp AspProSerVal ThrLeuGlu>

       960        970        980        990       1000
         *          *          *          *          *
CTGTCCCAGC TCTCCATGCT GCCCCACCTG GCTGACCTGG TCAGTTACAG
GACAGGGTCG AGAGGTACGA CGGGGTGGAC CGACTGGACC AGTCAATGTC
LeuSerGln LeuSerMetLeu ProHisLeu AlaAspLeu ValSerTyrSer>
```

Title: Isoforms of the Human Vitamin D Receptor
Inventor: Linda Anne Crofts
Application No.: 09/509,482
Docket No.: RICE-014

FIG 8C


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      1010       1020       1030       1040       1050
         *          *          *          *          *
 CATCCAAAAG GTCATTGGCT TTGCTAAGAT GATACCAGGA TTCAGAGACC
 GTAGGTTTTC CAGTAACCGA AACGATTCTA CTATGGTCCT AAGTCTCTGG
  IleGlnLys ValIleGly PheAlaLysMet IleProGly PheArgAsp>

      1060       1070       1080       1090       1100
         *          *          *          *          *
 TCACCTCTGA GGACCAGATC GTACTGCTGA AGTCAAGTGC CATTGAGGTC
 AGTGGAGACT CCTGGTCTAG CATGACGACT TCAGTTCACG GTAACTCCAG
LeuThrSerGlu AspGlnIle ValLeuLeu LysSerSerAla IleGluVal>

      1110       1120       1130       1140       1150
         *          *          *          *          *
 ATCATGTTGC GCTCCAATGA GTCCTTCACC ATGGACGACA TGTCCTGGAC
 TAGTACAACG CGAGGTTACT CAGGAAGTGG TACCTGCTGT ACAGGACCTG
 IleMetLeu ArgSerAsnGlu SerPheThr MetAspAsp MetSerTrpThr>

      1160       1170       1180       1190       1200
         *          *          *          *          *
 CTGTGGCAAC CAAGACTACA AGTACCGCGT CAGTGACGTG ACCAAAGCCG
 GACACCGTTG GTTCTGATGT TCATGGCGCA GTCACTGCAC TGGTTTCGGC
  CysGlyAsn GlnAspTyr LysTyrArgVal SerAspVal ThrLysAla>

      1210       1220       1230       1240       1250
         *          *          *          *          *
 GACACAGCCT GGAGCTGATT GAGCCCCTCA TCAAGTTCCA GGTGGGACTG
 CTGTGTCGGA CCTCGACTAA CTCGGGGAGT AGTTCAAGGT CCACCCTGAC
GlyHisSerLeu GluLeuIle GluProLeu IleLysPheGln ValGlyLeu>

      1260       1270       1280       1290       1300
         *          *          *          *          *
 AAGAAGCTGA ACTTGCATGA GGAGGAGCAT GTCCTGCTCA TGGCCATCTG
 TTCTTCGACT TGAACGTACT CCTCCTCGTA CAGGACGAGT ACCGGTAGAC
 LysLysLeu AsnLeuHisGlu GluGluHis ValLeuLeu MetAlaIleCys>

      1310       1320       1330       1340       1350
         *          *          *          *          *
 CATCGTCTCC CCAGATCGTC CTGGGGTGCA GGACGCCGCG CTGATTGAGG
 GTAGCAGAGG GGTCTAGCAG GACCCCACGT CCTGCGGCGC GACTAACTCC
  IleValSer ProAspArg ProGlyValGln AspAlaAla LeuIleGlu>

      1360       1370       1380       1390       1400
         *          *          *          *          *
 CCATCCAGGA CCGCCTGTCC AACACACTGC AGACGTACAT CCGCTGCCGC
 GGTAGGTCCT GGCGGACAGG TTGTGTGACG TCTGCATGTA GGCGACGGCG
AlaIleGlnAsp ArgLeuSer AsnThrLeu GlnThrTyrIle ArgCysArg>

      1410       1420       1430       1440       1450
         *          *          *          *          *
 CACCCGCCCC CGGGCAGCCA CCTGCTCTAT GCCAAGATGA TCCAGAAGCT
 GTGGGCGGGG GCCCGTCGGT GGACGAGATA CGGTTCTACT AGGTCTTCGA
 HisProPro ProGlySerHis LeuLeuTyr AlaLysMet IleGlnLysLeu>

      1460       1470       1480       1490       1500
         *          *          *          *          *
 AGCCGACCTG CGCAGCCTCA ATGAGGAGCA CTCCAAGCAG TACCGCTGCC
 TCGGCTGGAC GCGTCGGAGT TACTCCTCGT GAGGTTCGTC ATGGCGACGG
  AlaAspLeu ArgSerLeu AsnGluGluHis SerLysGln TyrArgCys>
```

FIG 8D ~~20/20~~

```
         1510         1520         1530         1540         1550
            *            *            *            *            *
 TCTCCTTCCA GCCTGAGTGC AGCATGAAGC TAACGCCCCT TGTGCTCGAA
 AGAGGAAGGT CGGACTCACG TCGTACTTCG ATTGCGGGGA ACACGAGCTT
LeuSerPheGln ProGluCys SerMetLys LeuThrProLeu ValLeuGlu>

         1560         1570
            *            *
 GTGTTTGGCA ATGAGATCTC CTGA (SEQ ID NO: 7)
 CACAAACCGT TACTCTAGAG GACT (SEQ ID NO: 20)
 ValPheGly AsnGluIleSer ***> (SEQ ID NO: 12)
```